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Claims:

1. A method of synthesizing a double stranded nucleic acid molecule comprising at least the steps of:
- 5 1) generating n double stranded nucleic acid fragments, wherein at least n-2 fragments have single stranded regions at both termini and 2 fragments have single stranded regions at at least one terminus, wherein (n-1) single stranded regions are complementary to (n-1) other
- 10 single stranded regions, thereby producing (n-1) complementary pairs,
- 2) contacting said n double stranded nucleic acid fragments, simultaneously or consecutively, to effect binding of said complementary pairs of single stranded
- 15 regions, and
- 3) optionally ligating said complementary pairs simultaneously or consecutively to produce a nucleic acid molecule consisting of n fragments, wherein said fragment comprises a region representing a
- 20 unit of information corresponding to one or more code elements and said code is alphanumeric.
2. A method of synthesizing a double stranded nucleic acid molecule comprising at least the steps of:
- 25 1) generating n double stranded nucleic acid fragments, wherein at least n-2 fragments have single stranded regions at both termini and 2 fragments have single stranded regions at at least one terminus, wherein (n-1) single stranded regions are complementary to (n-1) other
- 30 single stranded regions, thereby producing (n-1) complementary pairs,
- 2) contacting said n double stranded nucleic acid fragments, simultaneously or consecutively, to effect binding of said complementary pairs of single stranded
- 35 regions, and
- 3) optionally ligating said complementary pairs simultaneously or consecutively to produce a nucleic

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acid molecule consisting of n fragments,  
wherein said fragment comprises a region representing a  
unit of information corresponding to one or more code  
elements and said code is binary.

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3. A method of synthesizing a double stranded nucleic  
acid molecule comprising at least the steps of:

10 1) generating n double stranded nucleic acid fragments,  
wherein at least n-2 fragments have single stranded  
regions at both termini and 2 fragments have single  
stranded regions at at least one terminus, wherein (n-1)  
single stranded regions are complementary to (n-1) other  
single stranded regions, thereby producing (n-1)  
15 complementary pairs,

2) contacting said n double stranded nucleic acid  
fragments, simultaneously or consecutively, to effect  
binding of said complementary pairs of single stranded  
regions, and

20 3) optionally ligating said complementary pairs  
simultaneously or consecutively to produce a nucleic  
acid molecule consisting of n fragments,  
wherein said fragment comprises a region representing a  
unit of information corresponding to one or more code  
25 elements and each of said one or more code elements has  
the formula

$$(X)_a,$$

wherein

30 X is a nucleotide A, T, G, C or a derivative  
thereof which allows complementary binding and may be  
the same or different at each position, and

a is an integer from 4 to 10,  
wherein  $(X)_a$  is different for each one or more code  
elements.

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4. A method as claimed in claim 3 wherein said code is  
alphanumeric.

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5. A method as claimed in claim 3 wherein said code is binary.

6. A method as claimed in claim 5, wherein said code is binary and the code elements "1" and "0" have the formulae:

"0" =  $(X)_a$  and "1" =  $(Y)_b$ ,

wherein

10  $(X)_a$  and  $(Y)_b$  are not identical,

X and Y are each a nucleotide A, T, G, C or a derivative thereof which allows complementary binding and may be the same or different at each position, and a and b are integers from 4 to 10.

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7. A method as claimed in claim 6 wherein in the formulae  $(X)_a$  and  $(Y)_b$ , X and Y are the same at each position.

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8. A method as claimed in any one of claims 1 to 7 wherein said fragments are each between 8 and 25 bases in length.

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9. A method as claimed in any one of claims 1 to 8 wherein n is at least 10.

10. A method of synthesizing a double stranded nucleic acid molecule comprising at least the steps of:

30 1) generating fragment chains according to the method defined in any one of claims 1 to 9;

2) optionally generating single stranded regions at the end of said fragment chains, wherein said single stranded regions are complementary to the single stranded regions on said fragment chains thus forming complementary pairs of single stranded regions;

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3) contacting said fragment chains with one another, simultaneously or consecutively, to effect binding of

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said complementary pairs of single stranded regions.

11. A nucleic acid molecule produced according to a method as defined in any one of claims 1 to 10, or a single stranded nucleic acid molecule thereof.

12. A method of identifying the code elements contained in a nucleic acid molecule prepared according to a method as defined in any one of claims 1 to 10, wherein a probe, carrying a signalling means, specific to one or more code elements, is bound to said nucleic acid molecule and a signal generated by said signalling means is detected, whereby said one or more code elements may be identified.

13. A library of fragments as defined in any one of claims 1 to 12, comprising  $(n)_m$  fragments, wherein  $n$  is as defined in any one of claims 1 to 12 and corresponds to the length of chain that said library may produce, and  $m$  is an integer corresponding to the number of possible code elements or combinations thereof, such that fragments corresponding to all possible code elements for each position in the final chain are provided.

14. A kit for synthesizing a double stranded nucleic acid molecule comprising a library as defined in claim 13 and a ligase.